



Blast 2 Sequences results

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Taxonomy

Structure

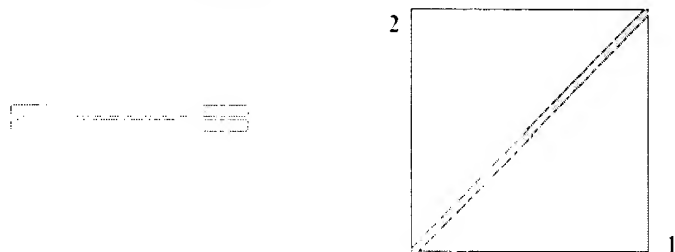
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

 Matrix: BLOSUM62 ☒ gap open: 11 gap extension: 1

x_dropoff: 3 expect: 300 wordsize: 3 Filter: Align

Sequence 1 gi: 2313 ATPase, H⁺-transporting, lysosomal, V0 subunit c: ATPase, H⁺-transporting, lysosomal 16kD, V0 subunit c: vacuolar proton pump, 16 kDa subunit: ATPase, H⁺-transporting, lysosomal, 16-KD: vacuolar ATP synthase 16 kDa proteolipid subunit: H⁺-transporting two-sector ATPase, 16 kDa subunit, vacuolar H⁺-ATPase proton channel subunit: ATPase, H⁺-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 gi: 29250 vacuolar ATPase 16kDa subunit c [Ovis aries] **Length 155 (1..155)**



The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 289 bits (721), Expect = 2e-75
 Identifier = 151/155 (97%), Positives = 153/155 (98%)

```

Query: 1  MDESHSGPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEQIMKSIIPVV 60
           MSE+HSGPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPE IMKSIIPVV
Sbjct: 1  MDEAHSGPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEMIMKSIIPVV 60

Query: 81  MAGHIAIYGLWAVLIANSINDDISLYKSFLQLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120
           MAGHIAIYGLWAVLIANSINDDISLYKSFLQLGAGLSVGLSGLAAGFAIGIVGDAGVRG
Sbjct: 81  MAGHIAIYGLWAVLIANSINDDISLYKSFLQLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120

Query: 131 TAQQPPLFVGHILTLIFAE'LGLYGLIIVALILSTK 155
           TAQQPPLFVGHILTLIFAE'LGLYGLIIVALILSTK
Sbjct: 131 TAQQPPLFVGHILTLIFAE'LGLYGLIIVALILSTK 155
  
```

Query time: 0.07 user secs. 0.03 sys. secs 0.10 total secs.

Query: 1 H
 Sbjct: 1 H
 0.140 0.381

Query: 1 H
 Sbjct: 1 H
 0.140 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 529

Number of Sequences: 0

Number of Extensions: 49

Number of Successful Extensions: 3

Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 155
length of database: 428,153,035
effective HSP length: 115
effective length of query: 40
effective length of database: 428,152,920
effective search space: 17126116800
effective search space used: 17126116800
T: 9
A: 40
X1: 15 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 40 (21.6 bits)
S2: 55 (25.8 bits)



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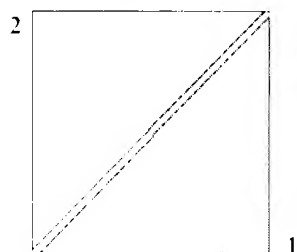
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

gap open: 11 gap extension: 1

x-dropoff: 1 expect: 300.0 wordsize: 3 Filter: Align

Sequence 1 gi: 10314 ATPase, H⁺-transporting, lysosomal, V0 subunit c; ATPase, H⁺-transporting, lysosomal 16kD, V0 subunit c; vacuolar proton pump, 16 kDa subunit; ATPase, H⁺-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H⁺-transporting two-sector ATPase, 16 kDa subunit; vacuolar H⁺-ATPase proton channel subunit; ATPase, H⁺-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 gi: 1477 Vacuolar ATP synthase 16 kDa proteolipid subunit *Bovine* **Length 155 (1..155)**



The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1371 bits (7118), Expect = 4e-75

Identical = 150/155 (96%), Positives = 153/155 (97%)

```

1  MSESKSGPEYASFFAVMGASAAMVFSALGAAAGTAKSGTGIAAMSVMPPEQIMKS
2  MBE+K+GPEYASFFAVMGASAAMVFSALGAAAGTAKSGTGIAAMSVMPPEIMKS
3  MBEAKNGPEYASFFAVMGASAAMVFSALGAAAGTAKSGTGIAAMSVMPPEMIMKS
4  ****
5  ****
6  ****
7  ****
8  ****
9  ****
10 ****
11 ****
12 ****
13 ****
14 ****
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143 ****
144 ****
145 ****
146 ****
147 ****
148 ****
149 ****
150 ****
151 ****
152 ****
153 ****
154 ****
155 ****

```

CPU time: 0.07 user secs. 0.03 sys. secs 0.10 total secs.

Lambda	K	H
0.325	0.141	0.382

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 527

Number of Sequences: 3

Number of extensions: 49

Number of successful extensions: 3

Number of sequences better than 300.0: 1

Number of HSP's better than 300.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non prelim): 1

length of query: 155

length of database: 423,153,035

effective HSP length: 115

effective length of query: 40

effective length of database: 426,152,920

effective search space: 17126116800

effective search space used: 17126116800

T: 3

A: 40

K1: 15 (7.0 bits)

K2: 129 (49.7 bits)

K3: 129 (49.7 bits)

S1: 40 (21.6 bits)

S2: 55 (25.8 bits)



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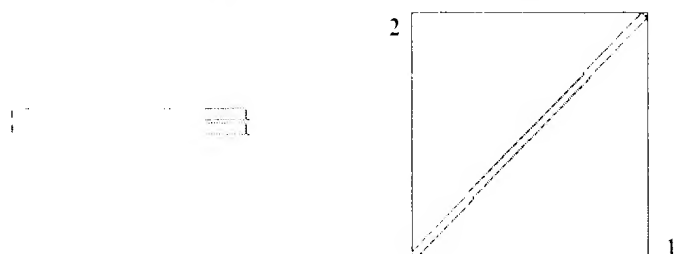
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix: BLO62-162 ☒ gap open: 11 gap extension: 1
 x-dropoff: 1 expect: 300 wordsize: 3 Filter: Align

Sequence 1 (gi: 10331) ATPase, H⁺-transporting, lysosomal, V0 subunit c; ATPase, H⁺-transporting, lysosomal 16kD, V0 subunit c; vacuolar proton pump, 16 kDa subunit; ATPase, H⁺-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H⁺-transporting two-sector ATPase, 16 kDa subunit, vacuolar H⁺-ATPase proton channel subunit; ATPase, H⁺-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 (gi: 2919) H-ATPase 16K *Bovine* **Length 154 (1..154)**



The statistics (bit score and expect value) is calculated based on the size of nr database

Score = 177 bits (708), Expect = 5e-74
 Identities = 148/153 (96%), Positives = 151/153 (97%)

```

1 10331      1  MDESKSGPEYASFFAVMGCASAAMVFSALGAAAYGTAKSGTGIAAMSVMRPEQIMKSIIPVV 60
2 2919      1  MDE+K+GPEYASFFAVMGCASAAMVFSALGAAAYGTAKSGTGIAAMSVMRPE IMKSIIPVV
1 10331      1  MDEAKNGPEYASFFAVMGCASAAMVFSALGAAAYGTAKSGTGIAAMSVMRPEMIMKSIIPVV 60
2 2919      1  MDEAKNGPEYASFFAVMGCASAAMVFSALGAAAYGTAKSGTGIAAMSVMRPEMIMKSIIPVV 60

1 10331     61  MNGIIAIYGLVAVLIANSLNDDISLYKSFLLGLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120
2 2919     61  MNGIIAIYGLVAVLIANSLNDDISLYKSFLLGLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120
1 10331     61  MNGIIAIYGLVAVLIANSLNDDISLYKSFLLGLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120
2 2919     61  MNGIIAIYGLVAVLIANSLNDDISLYKSFLLGLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120

1 10331    121  LAQOPPLFVGMILILIFAEVLGLYGLIVALILS 153
2 2919    121  LAQOPPLFVGMILILIFAEVLGLYGLIVALILS
1 10331    121  LAQOPPLFVGMILILIFAEVLGLYGLIVALILS 153
2 2919    121  LAQOPPLFVGMILILIFAEVLGLYGLIVALILS

```

Time: 0.04 user secs. 0.05 sys. secs 0.09 total secs.

Query: H H
 Score: 1.141 0.384

Query: H H
 Score: 0.410 0.140

Matrix: BLO62

Gap: 11 Existence: 11, Extension: 1

Number of hits to DB: 525

Number of sequences: 0

Number of extensions: 49

Number of successful extensions: 3

Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 154
length of database: 428,153,035
effective HSP length: 115
effective length of query: 39
effective length of database: 428,152,920
effective search space: 16697963880
effective search space used: 16697963880
T: 9
A: 40
X1: 15 (7.0 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 40 (21.6 bits)
S2: 55 (25.3 bits)



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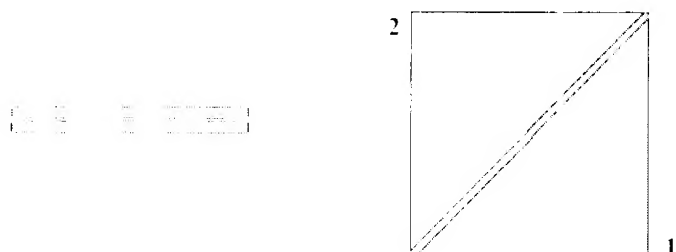
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Program: BLASTP ☒ gap open: 11 gap extension: 1
 Expect: 300.0 wordsize: 3 Filter: Align

Sequence 1 gi4502313 ATPase, H⁺-transporting, lysosomal, V0 subunit c; ATPase, H⁺-transporting, lysosomal 16kD, V0 subunit c; vacuolar proton pump, 16 kDa subunit; ATPase, H⁺-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H⁺-transporting two-sector ATPase, 16 kDa subunit; vacuolar H⁺-ATPase proton channel subunit; ATPase, H⁺-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 gi109937 H⁺-exporting ATPase (EC 3.6.3.6), vacuolar, 16K chain - mouse *mouse* **Length 155 (1..155)**



The statistics (bit score and expect value) is calculated based on the size of nr database

Score = 166 bits (680), Expect = 1e-70
 Identities = 147/155 (95%), Positives = 149/155 (95%)

```

Query: 1      MSESKSGPEYASFFAVMGASAAMVFSALGAAYGTAKSJTGIAAMSVMPFEQIMKSIIPVV 60
              M++ K+ PET+SFF VMGAS+AMVFSALGAAYGTAKSJTGIAAMSVMRFE IMKSIIPVV
Sbjct: 1      MADIENNPEYSSFFGVMGASSAMVFSAMGAAYGTAKSJTGIAAMSVMRFE LIMKSIIPVV 60

Query: 80      MAGIHAINGLTVAVLIANSLSNEDISLYHSFLQLGAGLSVGLSGLAAGFAIGIVGDA3VRG 120
              MAGIHAINGLTVAVLIANSLS E I+LY+SFLQLGAGLSVGLSGLAAGFAIGIVGDA3VRG
Sbjct: 67      MAGIHAINGLTVAVLIANSLSLDGITLYPSFLQLGAGLSVGLSGLAAGFAIGIVGDA3VRG 120

Query: 121     TAQOPPLFVGMILILFAEVLGLYGLIVALILITK 155
              TAQOPPLFVGMILILFAEVLGLYGLIVALILITK
Sbjct: 121     TAQOPPLFVGMILILFAEVLGLYGLIVALILITK 155
  
```

CPU time: 0.04 user secs. 0.05 sys. secs 0.09 total secs.

Lambda: K H
 0.141 0.141 0.387

Gap: G
 Lambda: F H
 0.047 0.0410 0.140

Matrix: BLOSUM62

Gap extension: Existence: 11, Extension: 1

Number of Hits to DB: 532

Number of Sequences: 0

Number of extensions: 51

Number of successful extensions: 3

Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 155
length of database: 428,153,035
effective HSP length: 115
effective length of query: 40
effective length of database: 428,152,920
effective search space: 17126116800
effective search space used: 17126116800
T: 9
A: 40
X1: 15 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 40 (21.6 bits)
S2: 55 (25.3 bits)

Blast 2 Sequences results

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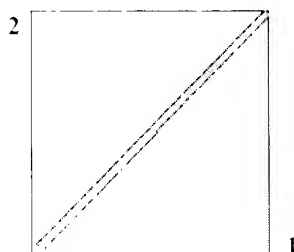
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

gap open: 11 gap extension: 1

x-dropoff: 2 expect: 300 wordsize: 2 Filter: Align

Sequence 1 gi: 12112 ATPase, H⁺-transporting, lysosomal, V0 subunit c; ATPase, H⁺-transporting, lysosomal 16kD, V0 subunit c, vacuolar proton pump, 16 kDa subunit; ATPase, H⁺-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H⁺-transporting two-sector ATPase, 16 kDa subunit, vacuolar H⁺-ATPase proton channel subunit; ATPase, H⁺-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 gi: 411 15 kDa protein [Torpedo marmorata] **Length 154 (1..154)**



The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 141 bits (671), Expect = 1e-69

Identities = 140/148 (94%), Positives = 145/148 (97%)



Query: 1 MNYASFFAVMGASAAMVFSALGAAYGTAKSSTGIAAMSVMRPEQIMKSIIPVVMAGIIAI 67

Ref: 1 MNY++FF V+GASAAMVFSALGAAYGTAKSSTGIAAMSVMRPE IMKSIIPVVMAGIIAI

Query: 2 MNYSAFFGVIGASAAMVFSALGAAYGTAKSSTGIAAMSVMRPELIMKSIIPVVMAGIIAI 66

Query: 127 YNLVWAVLIANSNLDELFLYKSFLLQGLSVGLSGLAAGFAIGIVGDAGVRGTAQQPRL 127

Ref: 127 YNLVWAVLIANSNL +DELFLYKSFLLQGLSVGLSGLAAGFAIGIVGDAGVRGTAQQPRL

Query: 126 YNLVWAVLIANSNLTEELFLKSFLLQGLSVGLSGLAAGFAIGIVGDAGVRGTAQQPRL 126

Query: 154 FTGMILILIFAENVLGLYGLIIVALILSTH 155

Ref: 154 FTGMILILIFAENVLGLYGLIIVALILSTH

Query: 153 FTGMILILIFAENVLGLYGLIIVALILSTH 154

Performance: 0.04 user secs. 0.05 sys. secs 0.09 total secs.

Length: 155 H
0.315 0.142 0.387

Gap: 0
Length: 155 H
0.000 0.0410 0.140

Database: BLAST

Number of hits: Existence: 11, Extension: 1

Number of hits to DB: 516

Number of sequences: 0

Number of extensions: 48

Number of successful extensions: 3

Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 154
length of database: 428,153,035
effective HSP length: 115
effective length of query: 39
effective length of database: 428,152,520
effective search space: 16697963880
effective search space used: 16697963880
T: 9
A: 40
X1: 15 (7.0 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 40 (21.6 bits)
S2: 55 (25.8 bits)

Number of successful extensions: 3
Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 154
length of database: 428,153,035
effective HSP length: 115
effective length of query: 39
effective length of database: 428,152,920
effective search space: 16697963880
effective search space used: 16697963880
T: 9
A: 40
X1: 15 (7.0 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 40 (21.5 bits)
S2: 55 (25.8 bits)

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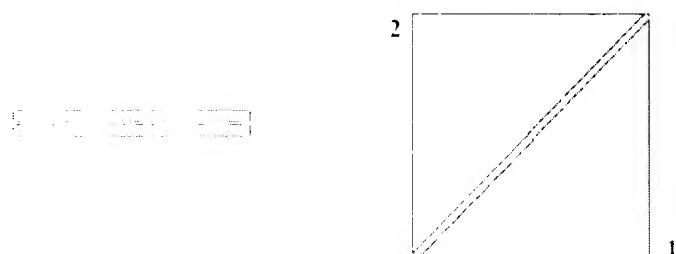
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix: BLOSUM62 ☒ gap open: 11 gap extension: 1

X-dropoff: 50 expect: 300 wordsize: 3 Filter: Align

Sequence 1 (gi: 6331) ATPase, H⁺-transporting, lysosomal, V0 subunit c; ATPase, H⁺-transporting, lysosomal 16kD, V0 subunit c; vacuolar proton pump, 16 kDa subunit; ATPase, H⁺-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H⁺-transporting two-sector ATPase, 16 kDa subunit, vacuolar H⁺-ATPase proton channel subunit; ATPase, H⁺-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 (gi: 954) H⁺-exporting ATPase (EC 3.6.3.6), vacuolar, 16K chain - bovine **Length 155 (1..155)**



The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 113 bits (646), Expect = 9e-67

Identities = 138/155 (89%), Positives = 143/155 (92%)

```

Query: 1  MESHSGPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEQIMKSIIPVV 60
           MEE+K+GPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPE IMKSIIPVV
Sbjct: 1  MSEAENGPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEMIMKSIIPVV 60

Query: 61  MAGHIAIYGLVVAVLIANSLNDGISLY+SFLQLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120
           MAGHIAIYGLVVAVLIANSLNDGISLY+SFLQLGAGLSVGLSGLAA ++G G
Sbjct: 61  MAGHIAIYGLVVAVLIANSLNDGISLY+SFLQLGAGLSVGLSGLAARSPSALLGTQGRAC 120

Query: 121  TAOQPPLFVGMILILIFAENVLGLYGLIVALILSTK 155
           TAOQPPLFVGMILILIFAENVLGLYGLIVALILSTK
Sbjct: 121  TAOQPPLFVGMILILIFAENVLGLYGLIVALILSTK 155

```

CPU time: 0.08 user secs. 0.00 sys. secs 0.08 total secs.

Length: 155 H
 0.24 0.138 0.375

Gaps: 0
 Length: 155 H
 0.07 0.0410 0.140

Matrix: BLOSUM62

Gap Penalty: Existence: 11, Extension: 1

Number of hits to DB: 490

Number of sequences: 0

Number of extensions: 42

Number of successful extensions: 3

Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non prelim): 1
length of query: 155
length of database: 428,153,035
effective HSP length: 115
effective length of query: 40
effective length of database: 428,152,920
effective search space: 17126116800
effective search space used: 17126116800
T: 9
A: 40
X1: 15 (7.0 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 40 (21.6 bits)
S2: 55 (25.8 bits)

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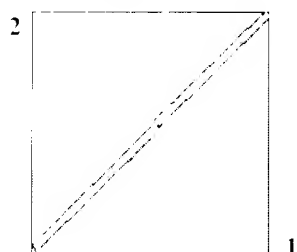
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix: BLOSUM62 ☐ gap open: 11 gap extension: 1

X-dropoff: 1 expect: 300.0 wordsize: 3 Filter: Align

Sequence 1 gi: 100000000.1
 ATPase, H⁺-transporting, lysosomal, V0 subunit c; ATPase, H⁺-transporting, lysosomal 16kD, V0 subunit c; vacuolar proton pump, 16 kDa subunit; ATPase, H⁺-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H⁺-transporting two-sector ATPase, 16 kDa subunit; vacuolar H⁺-ATPase proton channel subunit; ATPase, H⁺-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 gi: 100000000.2
 H⁺-ATPase [Drosophila melanogaster] **Length 159 (1..159)**



The statistics (bit score and expect value) is calculated based on the size of nr database

Score = 114 bits (593), Expect = 1e-60

Identical = 125/154 (81%), Positives = 135/154 (87%), Gaps = 2/154 (1%)

Query: 100000000.1
 Subject: 100000000.2

Query: 41 DSGPEYASFFAVMGASAAMVFSALGAAAYGTAKSSTGIAAMSVMRPEQIMKSIIPVVMAG 63
 Subject: 41 DSGPEYASFFAVMGASAAMVFSALGAAAYGTAKSSTGIAAMSVMRPEIMKSIIPVVMAG 63
 Query: 42 DSNPIYGPFFGVMGASAIIFSAALGAAAYGTAKSSTGIAAMSVMRPELIMKSIIPVVMAG 65
 Subject: 42 DSNPIYGPFFGVMGASAIIFSAALGAAAYGTAKSSTGIAAMSVMRPELIMKSIIPVVMAG 65
 Query: 121 LAIYGLVAVLIA +L + SLV+ F+ LGAGL+VG SGLAAGFAIGIVGLAQVRGT 121
 Subject: 121 LAIYGLVAVLIA +L + SLV+ F+ LGAGL+VG SGLAAGFAIGIVGLAQVRGT 125
 Query: 155 AQPPRLFVGMILILIFAEVLSGLYGLIVAILSTK 155
 Subject: 155 AQPPRLFVGMILILIFAEVLSGLYGLIVAILSTK 159
 Query: 159 AQPPRLFVGMILILIFAEVLSGLYGLIVAILYLYTK 159

CPU time: 0.06 user secs. 0.03 sys. secs 0.09 total secs.

Lambda: 0.1
 0.124 0.140 0.375

Gapped
 Lambda: 0.1
 0.124 0.140 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of hits to DB: 556

Number of sequences: 9

Number of extensions: 60

Number of successful extensions: 4

Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 155
length of database: 428,153,035
effective HSP length: 115
effective length of query: 40
effective length of database: 428,152,920
effective search space: 17126116800
effective search space used: 17126116800
T: 9
A: 40
X1: 15 (7.0 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (22.0 bits)
S2: 55 (25.8 bits)



PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
Search	Nucleotide	▼ for		Go Clear				
Limits		Preview/Index		History		Clipboard		Details
Display	default	▼ Show 20	▼ Send to	File	▼	Get Subsequence		

1: AC015913. Homo sapiens chro...[gi16506451]

Links

LOCUS AC015913 184595 bp DNA linear HTG 05-AUG-2002
DEFINITION Homo sapiens chromosome 17 clone RP11-81A22 map 17, WORKING DRAFT SEQUENCE, 32 unordered pieces.
ACCESSION AC015913
VERSION AC015913.3 GI:16506451
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 184595)
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 17, clone RP11-81A22
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 184595)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, H., Beckerly, R., Boguslavskiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, P., Gage, D., Galagan, J., Gardina, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, P., Jones, C., Kann, L., Karatas, A., Klein, J., Lehotzky, J., Lien, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, C., Naylor, T., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, E., Poltara, V., Piley, F., Roy, A., Santos, R., Severy, P., Stange Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (17 NOV 1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 184595)
AUTHORS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, H., Bastien, T., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S., Dodge, S., Fara, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardina, S., Gard, S., Graham, L., Grand Pierre, N., Hagos, B., Horton, L., Hume, W., Iliev, I., Johnson, P., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, T., Nguyen, C., Nicol, F., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, E., Phukhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, E., Stange Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodores, J., Trifam, E., Travers, H., Vassiliev, H., Vile, F., Vo, A., Wheeler, J., Wu, X., Wyman, D., Young, G., Zarnau, J., Zernich, D., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (06 AUG 2002) Whitehead Institute/MIT Center for Genome

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 27, 2001 this sequence version replaced gi:16356913.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L938
Center clone name: 31_A_21

----- Summary Statistics

Sequencing vector: M13; M77818; 40% of reads
Sequencing vector: Plasmid; n/a; 60% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Assembly program: Ehhap; version 0.960731
Consensus quality: 168221 bases at least Q40
Consensus quality: 175688 bases at least Q30
Consensus quality: 178768 bases at least Q20
Insert size: 203000; agarose-ff
Insert size: 181495; sum-of-contigs
Quality coverage: 7.6 in Q20 bases.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 11663: contig of 10663 bp in length
* 10664 10763: gap of 100 bp
* 10764 11392: contig of 628 bp in length
* 11393 11492: gap of 100 bp
* 11493 12333: contig of 840 bp in length
* 12334 12433: gap of 100 bp
* 12434 13333: contig of 899 bp in length
* 13334 13433: gap of 100 bp
* 13434 14716: contig of 1284 bp in length
* 14717 14816: gap of 100 bp
* 14817 16101: contig of 1285 bp in length
* 16102 16201: gap of 100 bp
* 16202 17397: contig of 1396 bp in length
* 17398 17497: gap of 100 bp
* 17498 18949: contig of 1451 bp in length
* 18950 19049: gap of 100 bp
* 19050 20494: contig of 1444 bp in length
* 20495 20594: gap of 100 bp
* 20595 21778: contig of 1183 bp in length
* 21779 21878: gap of 100 bp
* 21879 23459: contig of 1580 bp in length
* 23460 23559: gap of 100 bp
* 23560 25831: contig of 2272 bp in length
* 25832 25931: gap of 100 bp
* 25932 27763: contig of 1832 bp in length
* 27764 27863: gap of 100 bp
* 27864 29988: contig of 2124 bp in length
* 29989 30088: gap of 100 bp
* 30089 32675: contig of 2586 bp in length
* 32676 32775: gap of 100 bp
* 32776 36266: contig of 3491 bp in length
* 36267 36366: gap of 100 bp



Nucleotide

PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
Search	for						Go	Clear
Display	Show: 20	Send to	File		Get Subsequence			

1: AC015913 Homo sapiens chro...[gi:16506451]

1 of 5

LOCUS AC015913 184595 bp DNA linear HTG 05-AUG-2002
 DEFINITION Homo sapiens chromosome 17 clone RP11-81A22 map 17, WORKING DRAFT
 SEQUENCE, 30 unordered clones.

AC015913

AC015913.3 GI:16506451

KEYWORDS HTG; HTGS_PHASE1; HTGS_18AFT; HTGS_FULLTOP.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REPERENNIAL bases 1 to 184595

AUTHOR Pirren, E., Nisbaum, C. and Lander, E.

TITLE Homo sapiens chromosome 17, clone RP11-81A22

JOURNAL Unpublished

REPERENNIAL bases 1 to 184595

AUTHOR Pirren, E., Linton, L., Nisbaum, C., Lander, E., Allen, N., Anderson, M.,
 Balaban, J., Barna, N., Borkerly, R., Boguslavskiy, L., Bolikhgalter, B.,
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
 Cooke, P., DeArnelland, K., Dewar, K., Domino, M., Dorcelan, L., Doyle, M.,
 Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
 Galagan, J., Garayna, S., Grant, S., Haggis, B., Heaford, A., Horton, L.,
 Howland, J.C., Johnson, R., Jones, C., Kahr, L., Karatas, A., Klein, J.,
 Lehotzky, J., Liew, C., Locke, K., MacDonald, P., Marquis, N.,
 McEwan, B., McKinn, A., McVernan, K., McLaughlin, J., Melarim, J.,
 Morrow, C., Naylor, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
 Strange-Thomann, M., Stojanovic, N., Subramanian, A., Talamas, J.,
 Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, C., Wu, X.,
 Wyman, D., Ye, W.C., Zimmer, A. and Zody, M.

TITLE Direct Submission

JOURNAL Submitted (17 NOV 1999) Whitehead Institute/MIT Center for Genome
 Research, 300 Charles Street, Cambridge, MA 02141, USA

REPERENNIAL bases 1 to 184595

AUTHOR Pirren, E., Nisbaum, C., Lander, E., Allen, N., Anderson, S.,
 Barna, N., Bastien, M., Bloom, T., Boguslavskiy, L., Bolikhgalter, B.,
 Chamarata, J., Chang, C., Chazaro, B., Choepel, Y., Collymore, A.,
 Cooke, A., Cooke, P., DeArnelland, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Fano, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
 Garayna, S., Gerd, S., Graham, L., Grand Pierre, N., Haggis, B.,
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
 Karatas, A., Kelle, C., Lenders, T., Levine, R., Lindblad-Toh, K.,
 Liu, G., MacLean, C., MacDonald, P., Major, J., Matthews, C.,
 McCarthy, M., Melarim, J., Meneus, L., Minova, T., Klenga, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
 O'Connor, T., O'Donnell, P., O'Neil, E., Oliver, C., Peterson, K.,
 Phurkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P.,
 Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Talamas, J.,
 Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
 Viel, P., Vo, A., Wilson, J., Wu, X., Wyman, D., Young, G., Zainoun, J.,
 Zemzek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission

JOURNAL Submitted (06 AUG 2002) Whitehead Institute/MIT Center for Genome

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Oct 27, 2001 this sequence version replaced gi:1356913.
 All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://www.genome.wi.mit.edu/RepeatMasker.html>

Center: Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBB

Web site: <http://www.genome.wi.mit.edu>

Contact: sequence_submissions.genome.wi.mit.edu

Project Information

Center project name: L333

Center clone name: 31_A_12

Summary Statistics

Sequencing vector: M13; M77311; 41% of reads

Sequencing vector: Plasmid; r/a; 60% of reads

Chemistry: Dye-primer-amersham; 2% of reads

Chemistry: Dye-terminator Big Dye; 98% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 168221 bases at least Q40

Consensus quality: 175652 bases at least Q30

Consensus quality: 178769 bases at least Q20

Insert size: 21300; agarose-gel

Insert size: 181496; sum-of-contigs

Quality coverage: 7.6 in 220 bases.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 31 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 13663: contig of 13663 bp in length
 * 11364 11363: gap of 100 bp
 * 11364 11391: contig of 419 bp in length
 * 11391 11491: gap of 100 bp
 * 11491 11531: contig of 41 bp in length
 * 11531 12433: gap of 100 bp
 * 12433 12531: contig of 99 bp in length
 * 12531 14431: gap of 100 bp
 * 14431 14714: contig of 284 bp in length
 * 14714 14814: gap of 100 bp
 * 14814 16101: contig of 1287 bp in length
 * 16101 16201: gap of 100 bp
 * 16201 17797: contig of 1596 bp in length
 * 17797 17897: gap of 100 bp
 * 17897 18943: contig of 1051 bp in length
 * 18943 19043: gap of 100 bp
 * 19043 21494: contig of 1445 bp in length
 * 21494 21594: gap of 100 bp
 * 21594 21775: contig of 181 bp in length
 * 21775 21875: gap of 100 bp
 * 21875 23433: contig of 1554 bp in length
 * 23433 23533: gap of 100 bp
 * 23533 23831: contig of 1272 bp in length
 * 23831 23931: gap of 100 bp
 * 23931 27763: contig of 1832 bp in length
 * 27763 27863: gap of 100 bp
 * 27863 29986: contig of 2123 bp in length
 * 29986 30086: gap of 100 bp
 * 30086 32675: contig of 1589 bp in length
 * 32675 32775: gap of 100 bp
 * 32775 36266: contig of 3491 bp in length
 * 36266 36366: gap of 100 bp